

58049-00019.ST25

SEQUENCE LISTING

<110> Republic of National Fisheries Research and Development Institute
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KIM, Kyung Kil
LEE, Jong Yun
KONG, In Soo

<120> Phytase produced from Citrobacter braakii

<130> 58049-00019

<150> PCT/KR2004/000680
<151> 2004-03-25

<150> KR 10-2003-0018573
<151> 2003-03-25

<160> 8

<170> KopatentIn 1.71

<210> 1
<211> 1481
<212> DNA
<213> Citrobacter braakii YH-15

<220>
<221> MISC_FEATURE
<222> (1134)..(1134)
<223> n can be a, c, g or t

<400> 1
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ggaaactgcc cgatggaggg ggataactac tggaaacggg agctaatacc gcataacgtc 180
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ccagccacac tggaaactgag acacgggtcca gactcctacg ggaggcagca gtggggaata 360
ttgcacaatg ggcgcaagcc tgatgcagcc atgccgcgtg tatgaagaag gccttcgggt 420
tgtaaagtac tttcagcgag gaggaagggtg ttgtgggttaa taaccgcagc aattgacgtt 480
actcgcagaa gaagcaccgg ctaactccgt gccagcagcc gcggtataac ggagggtgca 540
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gggggtagaa ttccagggtg agcggtgaaa tgcgtagaga tctggaggaa taccggtggc 720
gaaggcggcc ccctggacaa agactgacgc tcagggtcga aagcgtgggg agcaaacagg 780
attagatacc ctggtagtcc acgccgtaaa cgatgtcgac ttggaggttg tgcccttgag 840
gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtacggc cgcaaggtta 900

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aaactcaaat gaattgacgg gggcccgac aagcgggtgga gcatgtggtt taattcgatg 960
 caacgcgaag aaccttacct actcttgaca tccagagaac ttagcagaga tgctttggtg 1020
 ccttcgggaa ctctgagaca ggtgctgcat ggctgtcgtc agctcgtgtt gtgaaatgtt 1080
 gggttaagtc ccgcaacgag cgcaaccctt atcctttgtt gccagcgggtt cggncgggaa 1140
 ctcaaaggag actgccagtg ataaactgga ggaaggtggg gatgacgtca agtcatcatg 1200
 gcccttacga gtagggctac acacgtgcta caatggcata taaaagaga agcgacctcg 1260
 cgagagcaag cggacctcat aaagtatgtc gtagtccgga ttggagtctg caactcgact 1320
 ccatgaagtc ggaatcgcta gtaatcgtgg atcagaatgc cacggtgaat acgttcccgg 1380
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 accttcggga gggcgcttac ctctttggat tcagatgggg a 1481

<210> 2
 <211> 10
 <212> PRT
 <213> *Citrobacter braakii* YH-15

<400> 2
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 1 5 10

<210> 3
 <211> 12
 <212> PRT
 <213> *Escherichia coli*

<400> 3
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 1 5 10

<210> 4
 <211> 15
 <212> PRT
 <213> *Aspergillus ficuum*

<400> 4
 Phe Ser Tyr Gly Ala Ala Ile Pro Gln Ser Thr Gln Glu Lys Gln
 1 5 10 15

<210> 5
 <211> 15
 <212> PRT
 <213> *Bacillus* sp.

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Xaa can be any natural amino acid

<400> 5

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Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Xaa Glu Thr Glu
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<210> 6
 <211> 1302
 <212> DNA
 <213> Citrobacter braakii YH-15

<220>
 <221> gene
 <222> (1)..(1302)
 <223> phytase gene

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 gtaagagcac ctacgaagtt cactccaata atgaaagatg tcacaccgga ccaatggcca 180
 caatgggatg tgccggttag atggctaacg cctcgtgggg gagaacttgt ttctgaatta 240
 ggtcagatc aacgtttatg gttcacaagc aaaggtctgt tgaataatca aacgtgcca 300
 tctccagggc aggttgctgt tattgcagac acggatcaac gcacccgtaa aacgggtgag 360
 gcgtttctgg ctggggttag accaaaatgt caaattcaag tgcattatca gaaggatgaa 420
 gaaaaaaaa atcctctttt taatccggta aaaatgggga aatgttcgtt taacacattg 480
 aagggttaaaa acgctattct ggaacgggcc ggaggaaata ttgaactgta taccacacgc 540
 tatcaatctt catttcggac cctggaaaat gttttaaatt tctcacaatc ggagacatgt 600
 aagactacag agaagtctac gaaatgcaca ttaccagagg ctttaccgtc tgaatttaag 660
 gtaactcctg acaacgtatc attacctggt gcctggagtc tttcttcac gctgactgag 720
 atatttctgt tgcaagaggc ccagggaatg ccacaggtag cctgggggagc tattacggga 780
 gaaaaagaat ggagagattt gtaagtctg cataacgctc agtttgatct ttgcaaaga 840
 actccagaag ttgcccgtag tagggccaca ccattactcg atatgataga cactgcatta 900
 ttgacaaatg gtacaacaga aaacaggtat ggcataaaat taccggtatc tctgttgttt 960
 attgctggtc atgataccaa tcttgcaaat ttaagcgggg ctttagatct taagtggctg 1020
 ctgcccggtc aacccgataa taccctcctt ggtggggagc ttgtattcga aaagtggaaa 1080
 agaaccagtg ataatacggg ttgggttcag gtttcatttg tttatcagac gctgagagat 1140
 atgaggggata ttcaaccgtt gtcgttagaa aaacctgctg gaaaagtga tttaaaatta 1200
 attgcatgtg aagagaaaaa tagtcaggga atgtgttcgt taaaaagttt ttccaggctc 1260
 attaaggaaa ttgcggtgcc agagtgtgca gttacggaat aa 1302

<210> 7
 <211> 433
 <212> PRT

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<213> Citrobacter braakii YH-15

<220>

<221> PEPTIDE

<222> (1)..(433)

<223> phytase

<400>

7

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 20 25 30
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Phe Thr
 35 40 45
 Pro Ile Met Lys Asp Val Thr Pro Asp Gln Trp Pro Gln Trp Asp Val
 50 55 60
 Pro Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Val Ser Glu Leu
 65 70 75 80
 Gly Gln Tyr Gln Arg Leu Trp Phe Thr Ser Lys Gly Leu Leu Asn Asn
 85 90 95
 Gln Thr Cys Pro Ser Pro Gly Gln Val Ala Val Ile Ala Asp Thr Asp
 100 105 110
 Gln Arg Thr Arg Lys Thr Gly Glu Ala Phe Leu Ala Gly Leu Ala Pro
 115 120 125
 Lys Cys Gln Ile Gln Val His Tyr Gln Lys Asp Glu Glu Lys Asn Asp
 130 135 140
 Pro Leu Phe Asn Pro Val Lys Met Gly Lys Cys Ser Phe Asn Thr Leu
 145 150 155 160
 Lys Val Lys Asn Ala Ile Leu Glu Arg Ala Gly Gly Asn Ile Glu Leu
 165 170 175
 Tyr Thr Gln Arg Tyr Gln Ser Ser Phe Arg Thr Leu Glu Asn Val Leu
 180 185 190
 Asn Phe Ser Gln Ser Glu Thr Cys Lys Thr Thr Glu Lys Ser Thr Lys
 195 200 205
 Cys Thr Leu Pro Glu Ala Leu Pro Ser Glu Phe Lys Val Thr Pro Asp
 210 215 220
 Asn Val Ser Leu Pro Gly Ala Trp Ser Leu Ser Ser Thr Leu Thr Glu
 225 230 235 240
 Ile Phe Leu Leu Gln Glu Ala Gln Gly Met Pro Gln Val Ala Trp Gly
 245 250 255
 Arg Ile Thr Gly Glu Lys Glu Trp Arg Asp Leu Leu Ser Leu His Asn
 260 265 270
 Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 275 280 285
 Ala Thr Pro Leu Leu Asp Met Ile Asp Thr Ala Leu Leu Thr Asn Gly

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300

290

295

Thr Thr Glu Asn Arg Tyr Gly Ile Lys Leu Pro Val Ser Leu Leu Phe
 305 310 315 320
 Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Ser Gly Ala Leu Asp
 325 330 335
 Leu Lys Trp Ser Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
 340 345 350
 Glu Leu Val Phe Glu Lys Trp Lys Arg Thr Ser Asp Asn Thr Asp Trp
 355 360 365
 Val Gln Val Ser Phe Val Tyr Gln Thr Leu Arg Asp Met Arg Asp Ile
 370 375 380
 Gln Pro Leu Ser Leu Glu Lys Pro Ala Gly Lys Val Asp Leu Lys Leu
 385 390 395 400
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 405 410 415
 Phe Ser Arg Leu Ile Lys Glu Ile Arg Val Pro Glu Cys Ala Val Thr
 420 425 430

Glu

<210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for the detection of phytase gene

<400> 8
 gargarcaga ayggyatgaa actggarcgy

30